Amendments to the Specification:

Please amend the specification by replacing the title with the following amended title:

METHODS FOR IDENTIFYING COMPOUNDS THAT INHIBIT CD38-ACTIVITY ~~MODULATED CHEMOTAXIS~~

Please amend the specification by replacing paragraph [0151] with the following amended paragraph:

Primers were made corresponding to the EST sequence found in Genbank accession #AW017229. (5' primer: acatctttgtggtactgaatggctcgg (SEQ ID NO:12) and 3' primer: tgagtaatgtctcgacgtttgacctcg (SEQ ID NO:13)) ~~(SEQ ID NOS:12-13)~~. *S. mansoni* cDNA libraries were obtained from Dr. Phillip LoVerde (SUNY, Buffalo), and were subjected to PCR using the primers indicated above. The library (1-20 µl) and dH2O were heated to 70^0C for 10 minutes and were then combined with the remainder of the PCR reagents and cycled. The cycles were: 95^0C 5 minutes, 1 cycle, followed by 95^0C 1 minute, 65^0C 1 minute and 72^0C 2 minutes for 35 cycles followed by 1 cycle at 72^0C for 5 minutes. The expected 330 bp band corresponding to EST AW017229 was isolated, TOPO cloned, and then used as a probe to screen 250,000 plaques from the *S. mansoni* cDNA library. Five positives were isolated and then subjected to 3 more rounds of screening in order to produce plaque pure clones. All five clones were fully sequenced on both strands. The nucleotide sequence and amino acid translation of four of the clones were identical (referred to as SM38). The stop codon and polyadenylation sites were identified in all of the SM38 clones, but the initiation methionine was not present in any of the clones. To obtain the 5' end of the SM38 gene, a single primer extension approach (NAR, 1994, vol 22, No. 16, p3427-3428) was utilized. A first round of PCR was performed using an external SM38 primer

(5' catcgaataaccctgatttcataacac) (SEQ ID NO:14) and the universal reverse primer for Bluescript. Two µl of this reaction was then subjected to PCR using an internal nested SM38 primer (5' gataaagtaagaactcgtgcc) (SEQ ID NO:15) and the universal reverse primer. A 200 and a 300 bp band were identified from this reaction and were directly sequenced. The sequence obtained overlapped 124 bp with the 5' end of the SM38 clones and included an additional 153 bp of sequence, however the no stop codon was detected, indicating that we still did not have the 5' end of the gene. Therefore, classic 5"RACE (PNAS vol 85 pp 8998-9002, Dec. 1998) was performed using ~~using~~ cDNA prepared from RNA isolated from adult *S. mansoni* worms (RNA provided by Dr. P. LoVerde, SUNY Buffalo). 10X Taq buffer, dNTP's, cDNA and Expand High Fidelity Taq were combined with the dT-AP primer (see ref. ~~For~~ for details) and cycled for 5 minutes at 95°C followed by 2 minutes at 50°C and 40 minutes at 72°C. After this 40 minute incubation the 5' external SM38 primer (see above) and AP primers were added and cycled for 35 cycles under the conditions: 95°C for 15 sec, 47°C for 30 sec, 72°C for 2 minutes followed by a 5 minute extension at 72°C. The reactions were run on a 1.5% agarose gel and a 300 bp band was isolated using Qiagen Gel Kit. The 5' RACE product was directly sequenced with the AP and 5' external SM38 primer. Two potential initiation methionines were identified in the sequence and two stop codons were found 13-19 amino acids upstream of the methionine residues. The RACE product was subsequently cloned. All three clones containing SM38 sequence (~~Two~~ two PCR generated clones and one clone from the S.mansoni cDNA library) were contiguous and overlapping. When assembled, the SM38 sequence included 1049 bp of sequence including 5' untranslated sequence, two potential initiation methionines, an open reading frame encoding a 303 amino acid protein, a stop codon, 3' untranslated sequence and a poly-adenylation site.